AMENDMENTS TO THE CLAIMS

1. **(Currently Amended)** Method for determining the susceptibility to antiviral drugs of HIV viruses in a biological sample comprising polynucleic acids, with said method comprising:

   a) ~~[if need be,]~~ releasing, isolating or concentrating the polynucleic acids present in the sample;

   b) ~~[if need be]~~ amplifying ~~[the relevant]~~ part of a protease gene of HIV comprising codons 82 and 84 from the polynucleic acids with at least one suitable primer pair;

   c) hybridizing the polynucleic acids of step a) or b) with ~~[at least two probes specifically hybridizing to a target sequence of the HIV protease gene, codon 82/84]~~ probes having the sequence of SEQ ID NO:267 and SEQ ID NO:354, or probes having sequence complementary to SEQ ID NO:267 and SEQ ID NO:354 ~~[the complement of said probe]~~;

   ~~[wherein said probes are capable of simultaneously hybridizing to their respective targets under appropriate hybridization and wash conditions;]~~

   wherein said probes are immobilized on a solid support; and

   d) inferring from the result of step c) whether or not a mutation giving rise to drug resistance is present in said target ~~[sequences]~~ sequence.

2. (Cancelled)

3. **(Currently Amended)** ~~[Method according to claim 1, further]~~ A method for determining the susceptibility to antiviral drugs of HIV viruses in a biological sample comprising polynucleic acids, with said method comprising:

   a) releasing, isolating or concentrating the polynucleic acids present in the sample;

   b) optionally, amplifying part of a protease gene of HIV comprising codons 82 and 84 with at least one suitable primer pair;

   c) hybridizing the polynucleic acids of step a) or b) with probes having the sequence of SEQ ID NO:267 and SEQ ID NO:354, or probes having sequences complementary to SEQ ID NO:267 and SEQ ID NO:354;

   wherein said probes are immobilized on a solid support; and

d) inferring from the result of step c) whether or not a mutation giving rise to drug resistance is present in said target sequence ~~[characterized in that said probes are chosen from the following list: SEQ ID NO: 228 to SEQ ID NO: 357, SEQ ID NO: 517 to SEQ ID NO: 519 or the complement of said probes]~~.

4. **(Currently Amended)** Method according to claim ~~[1]~~ 3 further characterized in that said primer pair is chosen from the following primers: SEQ ID NO: 3, SEQ ID NO: 503, SEQ ID NO: 504, SEQ ID NO: 4, SEQ ID NO: 506, SEQ ID NO: 507, SEQ ID NO: 508 and SEQ ID NO: 509.

5. **(Currently Amended)** ~~[Method according to]~~ The method of claim ~~[1]~~ 3 ~~[further characterized in that:]~~ wherein step b) comprises amplifying a fragment of the protease gene with at least one 5'-primer specifically hybridizing to a target sequence located at nucleotide position 210 to 260 of the coding portion of the protease gene, in combination with at least one suitable 3'-primer.

6. **(Currently Amended)** The method of claim ~~[1]~~ 3 ~~[further characterized in that:]~~ wherein step b) comprises amplifying a fragment of the protease gene with at least one 3'-primer specifically hybridizing to a target sequence located at nucleotide position 253 (codon 85) to position 300 of the coding portion of the protease gene, in combination with at least one suitable 5'-primer.

7. (Previously Presented) Method according to claim 5, further characterized in that the 5'-primer is SEQ ID NO: 5 and the 3'- primer is one primer or a combination of primers chosen from the following primers: SEQ ID NO: 4, SEQ ID NO: 506, SEQ ID NO: 507, SEQ ID NO: 508 and SEQ ID NO: 509.

8. (Previously Presented) Method according to claim 6, further characterized in that the 5'-primer is one primer or a combination of primers chosen from the following primers: SEQ ID NO: 3, SEQ ID NO: 503, SEQ ID NO: 504 and the 3'-primer is SEQ ID NO: 6.

9.–33. (Cancelled)

--34. **(New)** The method according to claim 1 wherein said primer pair is chosen from the following primers: SEQ ID NO: 3, SEQ ID NO: 503, SEQ ID NO: 504, SEQ ID NO: 4, SEQ ID NO: 506, SEQ ID NO: 507, SEQ ID NO: 508 and SEQ ID NO: 509.

35. **(New)** The method of claim 1 wherein step b) comprises amplifying a fragment of the protease gene with at least one 5'-primer specifically hybridizing to a target sequence located at nucleotide position 210 to 260 of the coding portion of the protease gene, in combination with at least one suitable 3'-primer.

36. **(New)** The method of claim 1 wherein step b) comprises amplifying a fragment of the protease gene with at least one 3'-primer specifically hybridizing to a target sequence located at nucleotide position 253 (codon 85) to position 300, in combination with at least one suitable 5'-primer.

37. **(New)** The method of claim 1 wherein the target sequences for codon 82/84 are provided by SEQ ID NO: 228–357.--